



SEQUENCE LISTING

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JUL 29 2002

TECH CENTER 1600/2900

B6  
<110> Hayward, Nicholas  
Silins, Ginters  
Grimmond, Sean  
Gartside, Michael  
Hancock, John

<120> THREE NOVEL GENES ENCODING A ZINC FINGER PROTEIN, A  
GUANINE, NUCLEOTIDE EXCHANGE FACTOR AND A HEAT SHOCK  
PROTEIN OR HEAT SHOCK BINDING PROTEIN

<130> 13198

<140> 09/424,458

<141> 2000-03-16

<150> PCT/AU98/00380

<151> 1998-05-22

<160> 125

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Peptide repeat  
motif in DnaJ homologues.

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Glu His Cys Leu Val Ala Asn His Ala Lys Cys Ile Val Gln Ser Tyr
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Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn Pro Asn Cys Arg Leu Cys
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Phe Pro Pro Thr Asn Leu Ala Gly Pro Val Ala Ser Ala Leu Arg Glu
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Thr Thr Arg Leu Val Cys Tyr Asp Leu Phe His Trp Ala Cys Leu Asn  
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Glu Arg Ala Ala Gln Leu Pro Arg Asn Thr Ala Pro Ala Gly Tyr Gln  
85 90 95

Cys Pro Ser Cys Asn Gly Pro Ile Phe Pro Pro Thr Asn Leu Ala Gly  
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115 120 125

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Pro Glu Pro Leu Asn Thr Ser Asp Phe Ser Asp Trp Ser Ser Phe Asn  
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Pro Ala Phe Tyr Ser Arg Ala Pro Arg Pro Pro Ala Ser Pro Gly Arg  
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Pro Glu Gln His Thr Val Ile His Met Gly Asn Pro Glu Pro Leu Thr  
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Ala	Ala	Ala	Asp	Ser	Asp	Pro	Asn	Leu	Asp	Pro	Leu	Met	Asn	Pro	His
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cca cgc ccc cga cct cca cta ggc ctg tgc cac ccg ctg cct gca gga 143

Pro	Arg	Pro	Arg	Pro	Pro	Leu	Gly	Leu	Cys	His	Pro	Leu	Pro	Ala	Gly
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cag gag gcg acc tcg tcc gcg ggt ttg cat tct ggg gtg gac gag ctg 287

Gln	Glu	Ala	Thr	Ser	Ser	Ala	Gly	Leu	His	Ser	Gly	Val	Asp	Glu	Leu
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 cca gcc cac ccc gcg ccg gcg gcc atg gca ggc acc ctg gac ctg gac 383  
 Pro Ala His Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp  
 115 120 125  
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 gat gac tcc ggg aag gtg cgg gac ccg cag ctg gtg cgc atg ttc ctc 479  
 Asp Asp Ser Gly Lys Val Arg Asp Pro Gln Leu Val Arg Met Phe Leu  
 145 150 155  
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 Met Met His Pro Trp Tyr Ile Pro Ser Ser Gln Leu Ala Ala Lys Leu  
 160 165 170 175  
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Leu Tyr Gln Leu Ser Leu Gln Arg Glu Pro Arg Ser Lys Ser Ser Pro	
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Thr Ser Pro Thr Ser Cys Thr Pro Pro Pro Arg Pro Pro Val Leu Glu	
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Ala Thr Gly Asn Tyr Gly Asn Tyr Arg Arg Arg Leu Ala Ala Cys Val

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Ser	Val	Ser	Leu	Glu	Gly	Ser	Ala	Pro	Ser	Pro	Ser	Pro	Met	His	Ser					
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tgtgccaccc gctgcctgca ggaagacgcc cgggtccggg ccgggtagc cccatgggaa 180  
  
cggggttcgg tccgagcccg gtgggaggct cccggagcgc agcctgggccc cagcccaccc 240  
  
cgcgccggcg gcc atg gca ggc acc ctg gac ctg gac aag ggc tgc acg 289  
Met Ala Gly Thr Leu Asp Leu Asp Lys Gly Cys Thr  
1 5 10  
gtg gag gag ctg ctc cgc ggg tgc atc gaa gcc ttc gat gac tcc ggg 337  
Val Glu Glu Leu Leu Arg Gly Cys Ile Glu Ala Phe Asp Asp Ser Gly  
15 20 25  
aag gtg cgg gac ccg cag ctg gtg cgc atg ttc ctc atg atg cac ccc 385  
Lys Val Arg Asp Pro Gln Leu Val Arg Met Phe Leu Met Met His Pro  
30 35 40  
tgg tac atc ccc tcc tct cag ctg gcg gcc aag ctg ctc cac atc tac 433  
Trp Tyr Ile Pro Ser Ser Gln Leu Ala Ala Lys Leu Leu His Ile Tyr  
45 50 55 60  
caa caa tcc cgg aag gac aac tcc aat tcc ctg cag gtg aaa acg tgc 481  
Gln Gln Ser Arg Lys Asp Asn Ser Asn Ser Leu Gln Val Lys Thr Cys  
65 70 75  
cac ctg gtc agg tac tgg atc tcc gcc ttc cca gcg gag ttt gac ttg 529  
His Leu Val Arg Tyr Trp Ile Ser Ala Phe Pro Ala Glu Phe Asp Leu  
80 85 90  
aac ccg gag ttg gct gag cag atc aag gag ctg aag gct ctg cta gac 577

Asn	Pro	Glu	Leu	Ala	Glu	Gln	Ile	Lys	Glu	Leu	Lys	Ala	Leu	Leu	Asp		
		95					100					105					
caa	gaa	ggg	aac	cga	cgg	cac	agc	agc	cta	atc	gac	ata	gac	agc	gtc	625	
Gln	Glu	Gly	Asn	Arg	Arg	His	Ser	Ser	Leu	Ile	Asp	Ile	Asp	Ser	Val		
	110					115					120						
cct	acc	tac	aag	tgg	aag	cgg	cag	gtg	act	cag	cgg	aac	cct	gtg	gga	673	
Pro	Thr	Tyr	Lys	Trp	Lys	Arg	Gln	Val	Thr	Gln	Arg	Asn	Pro	Val	Gly		
125					130					135					140		
cag	aaa	aag	cgc	aag	atg	tcc	ctg	ttg	ttt	gac	cac	ctg	gag	ccc	atg	721	
Gln	Lys	Lys	Arg	Lys	Met	Ser	Leu	Leu	Phe	Asp	His	Leu	Glu	Pro	Met		
				145					150					155			
gag	ctg	gcg	gag	cat	ctc	acc	tac	ttg	gag	tat	cgc	tcc	ttc	tgc	aag	769	
Glu	Leu	Ala	Glu	His	Leu	Thr	Tyr	Leu	Glu	Tyr	Arg	Ser	Phe	Cys	Lys		
		160						165					170				
atc	ctg	ttt	cag	gac	tat	cac	agt	ttc	gtg	act	cat	ggc	tgc	act	gtg	817	
Ile	Leu	Phe	Gln	Asp	Tyr	His	Ser	Phe	Val	Thr	His	Gly	Cys	Thr	Val		
		175					180					185					
gac	aac	ccc	gtc	ctg	gag	cgg	ttc	atc	tcc	ctc	ttc	aac	agc	gtc	tca	865	
Asp	Asn	Pro	Val	Leu	Glu	Arg	Phe	Ile	Ser	Leu	Phe	Asn	Ser	Val	Ser		
	190					195					200						
cag	tgg	gtg	cag	ctc	atg	atc	ctc	agc	aaa	ccc	aca	gcc	ccg	cag	cgg	913	
Gln	Trp	Val	Gln	Leu	Met	Ile	Leu	Ser	Lys	Pro	Thr	Ala	Pro	Gln	Arg		
205					210					215					220		
gcc	ctg	gtc	atc	aca	cac	ttt	gtc	cac	gtg	gcg	gag	aag	ctg	cta	cag	961	
Ala	Leu	Val	Ile	Thr	His	Phe	Val	His	Val	Ala	Glu	Lys	Leu	Leu	Gln		
				225					230					235			
ctg	cag	aac	ttc	aac	acg	ctg	atg	gca	gtg	gtc	ggg	ggc	ctg	agc	cac	1009	
Leu	Gln	Asn	Phe	Asn	Thr	Leu	Met	Ala	Val	Val	Gly	Gly	Leu	Ser	His		
			240					245					250				
agc	tcc	atc	tcc	cgc	ctc	aag	gag	acc	cac	agc	cac	gtt	agc	cct	gag	1057	
Ser	Ser	Ile	Ser	Arg	Leu	Lys	Glu	Thr	His	Ser	His	Val	Ser	Pro	Glu		
		255					260					265					
acc	atc	aag	ctc	tgg	gag	ggt	ctc	acg	gaa	cta	gtg	acg	gcg	aca	ggc	1105	
Thr	Ile	Lys	Leu	Trp	Glu	Gly	Leu	Thr	Glu	Leu	Val	Thr	Ala	Thr	Gly		
	270					275					280						

aac tat ggc aac tac cgg cgt cgg ctg gca gcc tgt gtg ggc ttc cgc	1153
Asn Tyr Gly Asn Tyr Arg Arg Arg Leu Ala Ala Cys Val Gly Phe Arg 285 290 295 300	
ttc ccg atc ctg ggt gtg cac ctc aag gac ctg gtg gcc ctg cag ctg	1201
Phe Pro Ile Leu Gly Val His Leu Lys Asp Leu Val Ala Leu Gln Leu 305 310 315	
gca ctg cct gac tgg ctg gac cca gcc cgg acc cgg ctc aac ggg gcc	1249
Ala Leu Pro Asp Trp Leu Asp Pro Ala Arg Thr Arg Leu Asn Gly Ala 320 325 330	
aag atg aag cag ctc ttt agc atc ctg gag gag ctg gcc atg gtg acc	1297
Lys Met Lys Gln Leu Phe Ser Ile Leu Glu Glu Leu Ala Met Val Thr 335 340 345	
agc ctg cgg cca cca gta cag gcc aac ccc gac ctg ctg agc ctg ctc	1345
Ser Leu Arg Pro Pro Val Gln Ala Asn Pro Asp Leu Leu Ser Leu Leu 350 355 360	
acg gtg tct ctg gat cag tat cag acg gag gat gag ctg tac cag ctg	1393
Thr Val Ser Leu Asp Gln Tyr Gln Thr Glu Asp Glu Leu Tyr Gln Leu 365 370 375 380	
tcc ctg cag cgg gag ccg cgc tcc aag tcc tcg cca acc agc ccc acg	1441
Ser Leu Gln Arg Glu Pro Arg Ser Lys Ser Ser Pro Thr Ser Pro Thr 385 390 395	
agt tgc acc cca cca ccc cgg ccc ccg gta ctg gag gag tgg acc tcg	1489
Ser Cys Thr Pro Pro Pro Arg Pro Pro Val Leu Glu Glu Trp Thr Ser 400 405 410	
gct gcc aaa ccc aag ctg gat cag gcc ctc gtg gtg gag cac atc gag	1537
Ala Ala Lys Pro Lys Leu Asp Gln Ala Leu Val Val Glu His Ile Glu 415 420 425	
aag atg gtg gag tct gtg ttc cgg aac ttt gac gtc gat ggg gat ggc	1585
Lys Met Val Glu Ser Val Phe Arg Asn Phe Asp Val Asp Gly Asp Gly 430 435 440	
cac atc tca cag gaa gaa ttc cag atc atc cgt ggg aac ttc cct tac	1633
His Ile Ser Gln Glu Glu Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr 445 450 455 460	
ctc agc gcc ttt ggg gac ctc gac cag aac cag gat ggc tgc atc agc	1681
Leu Ser Ala Phe Gly Asp Leu Asp Gln Asn Gln Asp Gly Cys Ile Ser 465 470 475	

agg gag gag atg gtt tcc tat ttc ctg cgc tcc agc tct gtg ttg ggg 1729  
Arg Glu Glu Met Val Ser Tyr Phe Leu Arg Ser Ser Ser Val Leu Gly  
480 485 490

ggg cgc atg ggc ttc gta cac aac ttc cag gag agc aac tcc ttg cgc 1777  
Gly Arg Met Gly Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg  
495 500 505

ccc gtc gcc tgc cgc cac tgc aaa gcc ctg atc ctg ggc atc tac aag 1825  
Pro Val Ala Cys Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys  
510 515 520

Bb cag ggc ctc aaa tgc cga gcc tgt gga gtg aac tgc cac aag cag tgc 1873  
Gln Gly Leu Lys Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys  
525 530 535 540

aag gat cgc ctg tca gtt gag tgt cgg cgc agg gcc cag agt gtg agc 1921  
Lys Asp Arg Leu Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser  
545 550 555

ctg gag ggg tct gca ccc tca ccc tca ccc atg cac agc cac cat cac 1969  
Leu Glu Gly Ser Ala Pro Ser Pro Ser Pro Met His Ser His His His  
560 565 570

cgc gcc ttc agc ttc tct ctg ccc cgc cct ggc agg cga ggc tcc agg 2017  
Arg Ala Phe Ser Phe Ser Leu Pro Arg Pro Gly Arg Arg Gly Ser Arg  
575 580 585

cct cca gag atc cgt gag gag gag gta cag acg gtg gag gat ggg gtg 2065  
Pro Pro Glu Ile Arg Glu Glu Glu Val Gln Thr Val Glu Asp Gly Val  
590 595 600

ttt gac atc cac ttg taatagatgc tgtggttgga tcaaggactc attcctgcct 2120  
Phe Asp Ile His Leu  
605

tggagaaaat acttcaacca gagcagggag cctgggggtg tcggggcagg aggctgggga 2180

tggggggtggg atatgagggt ggcattgcagc tgagggcagg gccagggctg gtgtccctaa 2240

ggttgtacag actcttgtga atatttgtat tttccagatg gaataaaaag gcccggtgtaa 2300

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 <211> 609  
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 <213> Homo sapiens

<400> 7

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			20					25					30		
Pro	Gln	Leu	Val	Arg	Met	Phe	Leu	Met	Met	His	Pro	Trp	Tyr	Ile	Pro
		35					40					45			
Ser	Ser	Gln	Leu	Ala	Ala	Lys	Leu	Leu	His	Ile	Tyr	Gln	Gln	Ser	Arg
	50					55					60				
Lys	Asp	Asn	Ser	Asn	Ser	Leu	Gln	Val	Lys	Thr	Cys	His	Leu	Val	Arg
65					70					75					80
Tyr	Trp	Ile	Ser	Ala	Phe	Pro	Ala	Glu	Phe	Asp	Leu	Asn	Pro	Glu	Leu
				85					90					95	
Ala	Glu	Gln	Ile	Lys	Glu	Leu	Lys	Ala	Leu	Leu	Asp	Gln	Glu	Gly	Asn
			100					105					110		
Arg	Arg	His	Ser	Ser	Leu	Ile	Asp	Ile	Asp	Ser	Val	Pro	Thr	Tyr	Lys
		115					120					125			
Trp	Lys	Arg	Gln	Val	Thr	Gln	Arg	Asn	Pro	Val	Gly	Gln	Lys	Lys	Arg
	130					135					140				
Lys	Met	Ser	Leu	Leu	Phe	Asp	His	Leu	Glu	Pro	Met	Glu	Leu	Ala	Glu
145					150					155					160
His	Leu	Thr	Tyr	Leu	Glu	Tyr	Arg	Ser	Phe	Cys	Lys	Ile	Leu	Phe	Gln
				165					170					175	
Asp	Tyr	His	Ser	Phe	Val	Thr	His	Gly	Cys	Thr	Val	Asp	Asn	Pro	Val
			180					185					190		
Leu	Glu	Arg	Phe	Ile	Ser	Leu	Phe	Asn	Ser	Val	Ser	Gln	Trp	Val	Gln
		195					200					205			
Leu	Met	Ile	Leu	Ser	Lys	Pro	Thr	Ala	Pro	Gln	Arg	Ala	Leu	Val	Ile
	210					215					220				
Thr	His	Phe	Val	His	Val	Ala	Glu	Lys	Leu	Leu	Gln	Leu	Gln	Asn	Phe
225					230					235					240
Asn	Thr	Leu	Met	Ala	Val	Val	Gly	Gly	Leu	Ser	His	Ser	Ser	Ile	Ser
				245					250					255	
Arg	Leu	Lys	Glu	Thr	His	Ser	His	Val	Ser	Pro	Glu	Thr	Ile	Lys	Leu
			260					265					270		



Trp Glu Gly Leu Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Gly Asn  
 275 280 285  
 Tyr Arg Arg Arg Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu  
 290 295 300  
 Gly Val His Leu Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp  
 305 310 315 320  
 Trp Leu Asp Pro Ala Arg Thr Arg Leu Asn Gly Ala Lys Met Lys Gln  
 325 330 335  
 Leu Phe Ser Ile Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro  
 340 345 350  
 Pro Val Gln Ala Asn Pro Asp Leu Leu Ser Leu Leu Thr Val Ser Leu  
 355 360 365  
 Asp Gln Tyr Gln Thr Glu Asp Glu Leu Tyr Gln Leu Ser Leu Gln Arg  
 370 375 380  
 Glu Pro Arg Ser Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro  
 385 390 395 400  
 Pro Pro Arg Pro Pro Val Leu Glu Glu Trp Thr Ser Ala Ala Lys Pro  
 405 410 415  
 Lys Leu Asp Gln Ala Leu Val Val Glu His Ile Glu Lys Met Val Glu  
 420 425 430  
 Ser Val Phe Arg Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln  
 435 440 445  
 Glu Glu Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe  
 450 455 460  
 Gly Asp Leu Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met  
 465 470 475 480  
 Val Ser Tyr Phe Leu Arg Ser Ser Ser Val Leu Gly Gly Arg Met Gly  
 485 490 495  
 Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys  
 500 505 510  
 Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys  
 515 520 525  
 Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu  
 530 535 540  
 Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser  
 545 550 555 560  
 Ala Pro Ser Pro Ser Pro Met His Ser His His His Arg Ala Phe Ser  
 565 570 575  
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Arg Glu Glu Glu Val Gln Thr Val Glu Asp Gly Val Phe Asp Ile His		
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Leu

<210> 8  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
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ccc cgc aac cct ccc tcc cgg ctc ctc gga gcg gcc gcc ggg cag cgg	97
Pro Arg Asn Pro Pro Ser Arg Leu Leu Gly Ala Ala Ala Gly Gln Arg	
15 20 25	
tcc aga ccc agt act tat tat gaa ctg ttg ggg gtg cat cct ggt gcc	145
Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala	
30 35 40 45	
agc act gag gaa gtt aaa cga gct ttc ttc tcc aag tcc aaa gag ctg	193
Ser Thr Glu Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu	
50 55 60	
cac cca gac cgg gac cct ggg aac cca agc ctg cac agc cgc ttt gtg	241
His Pro Asp Arg Asp Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val	
65 70 75	
gag ctg agc gag gca tac cgt gtg ctc agc cgt gag cag agc cgc cgc	289
Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln Ser Arg Arg	
80 85 90	
agc tat gat gac cag ctc cgc tca ggt agt ccc cca aag tct cca cga	337
Ser Tyr Asp Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys Ser Pro Arg	
95 100 105	
acc aca gtc cat gac aag tct gcc cac caa aca cac agc tcc tgg aca	385
Thr Thr Val His Asp Lys Ser Ala His Gln Thr His Ser Ser Trp Thr	
110 115 120 125	

ccc ccc aac gca cag tac tgg tcc cag ttt cac agc gtg agg cca cag 433  
Pro Pro Asn Ala Gln Tyr Trp Ser Gln Phe His Ser Val Arg Pro Gln  
130 135 140  
ggg ccc cag ttg agg cag cag caa cac aaa caa aac aaa caa gtg ctg 481  
Gly Pro Gln Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln Val Leu  
145 150 155  
ggg tac tgc ctc ctc ctc atg ctg gcg ggc atg ggc ctg cac tac att 529  
Gly Tyr Cys Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile  
160 165 170  
gcc ttc agg aag gtg aag cag atg cac ctt aac ttc atg gat gaa aag 577  
Ala Phe Arg Lys Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys  
175 180 185  
gat cgg atc atc aca gcc ttc tac aac gaa gcc cgg gca cgg gcc agg 625  
Asp Arg Ile Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg  
190 195 200 205  
gcc aac aga ggc atc ctt cag cag gag cga caa cgg cta ggg cag cgg 673  
Ala Asn Arg Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu Gly Gln Arg  
210 215 220  
cag ccg cca cca tcc gag cca acc caa ggc ccc gag atc gtg ccc cgg 721  
Gln Pro Pro Pro Ser Glu Pro Thr Gln Gly Pro Glu Ile Val Pro Arg  
225 230 235  
ggc gcc ggc ccc tgaggggctc acctggatgg ggctgcagt gcgttcccgc 773  
Gly Ala Gly Pro  
240  
tttgcttctt tccctggacg gcccgctccc cgaaacgcgc gcaataaagt gattcgcag 832

<210> 9  
<211> 241  
<212> PRT  
<213> Homo sapiens

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Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu  
35 40 45

Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp  
 50 55 60  
 Arg Asp Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val Glu Leu Ser  
 65 70 75 80  
 Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln Ser Arg Arg Ser Tyr Asp  
 85 90 95  
 Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys Ser Pro Arg Thr Thr Val  
 100 105 110  
 His Asp Lys Ser Ala His Gln Thr His Ser Ser Trp Thr Pro Pro Asn  
 115 120 125  
 Ala Gln Tyr Trp Ser Gln Phe His Ser Val Arg Pro Gln Gly Pro Gln  
 130 135 140  
 Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln Val Leu Gly Tyr Cys  
 145 150 155 160  
 Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile Ala Phe Arg  
 165 170 175  
 Lys Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys Asp Arg Ile  
 180 185 190  
 Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg Ala Asn Arg  
 195 200 205  
 Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu Gly Gln Arg Gln Pro Pro  
 210 215 220  
 Pro Ser Glu Pro Thr Gln Gly Pro Glu Ile Val Pro Arg Gly Ala Gly  
 225 230 235 240

Pro

<210> 10  
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<400> 10  
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 1 5 10

<210> 11  
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 <212> PRT  
 <213> Homo sapiens

<400> 11  
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 1 5 10

<210> 12  
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<400> 12  
 Asp His Asp Arg Asp Gly Phe Ile Ser Gln Glu Glu Phe  
 1 5 10

<210> 13  
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 <212> PRT  
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 1 5 10

<210> 14  
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 <213> C. elegans

<400> 14  
 Asp Val Asp Met Asp Gly Gln Ile Ser Lys Asp Glu Leu  
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<210> 15  
 <211> 37  
 <212> PRT  
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<400> 15  
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 Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser Arg  
 20 25 30  
 Leu Lys Glu Thr His  
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<210> 16  
 <211> 37  
 <212> PRT  
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<400> 16  
 Lys Phe Val His Val Ala Lys His Leu Arg Lys Ile Asn Asn Phe Asn  
 1 5 10 15

Thr Leu Met Ser Val Val Gly Gly Ile Thr His Ser Ser Val Ala Arg  
 20 25 30

Leu Ala Lys Thr Tyr  
 35

<210> 17  
 <211> 50  
 <212> PRT  
 <213> Homo sapiens

<400> 17  
 His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys Arg His  
 1 5 10 15

Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys Cys Arg  
 20 25 30

Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu Ser Val  
 35 40 45

Glu Cys  
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<210> 18  
 <211> 50  
 <212> PRT  
 <213> C. elegans

<400> 18  
 His Asn Phe His Glu Thr Thr Phe Leu Thr Pro Thr Thr Cys Asn His  
 1 5 10 15

Cys Asn Lys Leu Leu Trp Gly Ile Leu Arg Gln Gly Phe Lys Cys Lys  
 20 25 30

Asp Cys Gly Leu Ala Val His Ser Cys Cys Lys Ser Asn Ala Val Ala  
 35 40 45

Glu Cys  
 50

<210> 19  
 <211> 15  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 sequence of pGEX and mcg7 junction.

<400> 19  
 gggatcccc tggtc

15

<210> 20  
<211> 21  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:Nucleotide  
sequence of pGEX and mcg7 junction.

<400> 20  
gaattcggca cgagccgacg g

21

<210> 21  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Nucleotide  
sequence of myc-tag/mcg7 junction.

<400> 21  
atggagcaga agctgatctc cgaggaggac ctgcccgggg cagctggatc cgcagcccac 60  
cccgcgccgg cggccatg 78

<210> 22  
<211> 26  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:The amino acid  
sequence encoded by the nucleotide sequence of SEQ  
ID NO: 21.

<400> 22  
Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Pro Gly Ala Ala Gly  
1 5 10 15  
Ser Ala Ala His Pro Ala Pro Ala Ala Met  
20 25

<210> 23  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Nucleotide  
sequence of pGEX and mcg7 junction.

<400> 23  
ggatccgcag cccaccccgcc gccggcggcc atg

33

<210> 24  
<211> 11  
<212> PRT  
<213> Artificial Sequence

bb <220>  
<223> Description of Artificial Sequence: The amino acid  
sequence encoded by the nucleotide sequence of SEQ  
ID NO: 23.

<400> 24  
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1 5 10

<210> 25  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mcg-7 specific  
oligonucleotide.

<400> 25  
ggacaaagtg tgtgatgaac c 21

<210> 26  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mcg-7 specific  
oligonucleotide.

<400> 26  
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<210> 27  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mcg-18 specific  
oligonucleotide.

<400> 27  
gtagatgtgg atcagcttgg 20



<210> 28  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mcg-18 specific  
oligonucleotide.

<400> 28  
aggtggagaa tgggtcaagg 19

<210> 29  
<211> 20  
<212> DNA  
<213> Artificial Sequence

B6  
<220>  
<223> Description of Artificial Sequence:mcg-18 specific  
oligonucleotide.

<400> 29  
gtcatagtct gtctcctact 20

<210> 30  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mcg-18 specific  
oligonucleotide.

<400> 30  
acatagacag cgtgcctacc 20

<210> 31  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mcg-18 specific  
oligonucleotide.

<400> 31  
tacaacctta gggacaccag 20

<210> 32  
<211> 20

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
         oligonucleotide.  
  
 <400> 32  
 tgctgagcct gctcacggtg 20  
  
  
 <210> 33  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
         oligonucleotide.  
  
 <400> 33  
 caagtgaaca gcacgtcc 18  
  
  
 <210> 34  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
         oligonucleotide  
  
 <400> 34  
 gactatctca aggaccagct g 21  
  
  
 <210> 35  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
         oligonucleotide.  
  
 <400> 35  
 ggttcgtcc gagcccgg 18  
  
  
 <210> 36  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 36  
 ggagcgatac tccaagtagg t 21

<210> 37  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 37  
 agcgggccag gccccttc 18

<210> 38  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 38  
 catcctggtc caatgcgctc 20

<210> 39  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 39  
 gcactgagga agttaaacga gc 22

<210> 40  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 40  
gctcggttaa cttcctcagt gc 22

<210> 41  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mcg-18 specific  
oligonucleotide.

<400> 41  
gctcagctcc acaaagcggc t 21

<210> 42  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mcg-18 specific  
oligonucleotide.

<400> 42  
accagctccg ctcaggtag 19

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mcg-18 specific  
oligonucleotide.

<400> 43  
tccaggagct gtgtgtttgg 20

<210> 44  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mcg-18 specific  
oligonucleotide.

<400> 44  
ccagtttcac agcgtgagg 19

<210> 45  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mcg-18 specific  
oligonucleotide.

<400> 45  
cagcatgagg aggaggcag

19

<210> 46  
<211> 60  
<212> PRT  
<213> Homo sapiens

<400> 46  
Met Gly Leu Cys Lys Cys Pro Lys Arg Lys Val Thr Asn Leu Phe Cys  
1 5 10 15  
Phe Glu His Arg Val Asn Val Cys Glu His Cys Leu Val Ala Asn His  
20 25 30  
Ala Lys Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp  
35 40 45  
Tyr Asn Pro Asn Cys Arg Leu Cys Asn Ile Pro Leu  
50 55 60

<210> 47  
<211> 60  
<212> PRT  
<213> Mus musculus

<400> 47  
Met Gly Leu Cys Lys Cys Pro Lys Arg Lys Val Thr Asn Leu Phe Cys  
1 5 10 15  
Phe Glu His Arg Val Asn Val Cys Glu His Cys Leu Val Ala Asn His  
20 25 30  
Ala Lys Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp  
35 40 45  
Tyr Asn Pro Asn Cys Arg Leu Cys Asn Thr Pro Leu  
50 55 60

<210> 48  
<211> 103  
<212> PRT  
<213> Homo sapiens

<400> 48

Pro Lys Arg Lys Val Thr Asn Leu Phe Cys Phe Glu His Arg Val Asn  
1 5 10 15

Val Cys Glu His Cys Leu Val Ala Asn His Ala Lys Cys Ile Val Gln  
20 25 30

Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn Pro Asn Cys Arg  
35 40 45

Leu Cys Asn Ile Pro Leu Ala Ser Arg Glu Thr Thr Arg Leu Val Cys  
50 55 60

Tyr Asp Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu  
65 70 75 80

Pro Arg Asn Thr Ala Pro Ala Gly Tyr Gln Cys Pro Ser Cys Asn Gly  
85 90 95

Pro Ile Phe Pro Pro Asn Gln  
100

<210> 49

<211> 103

<212> PRT

<213> C. elegans

<220>

<221> UNSURE

<222> (10)

<223> Xaa at position 10 can be any amino acid.

<220>

<221> UNSURE

<222> (21)

<223> Xaa at position 21 can be any amino acid.

<220>

<221> UNSURE

<222> (55)

<223> Xaa at position 55 can be any amino acid.

<220>

<221> UNSURE

<222> (77)

<223> Xaa at position 77 can be any amino acid.

<220>

<221> UNSURE

<222> (87)

<223> Xaa at position 87 can be any amino acid.

<400> 49

Pro Lys Arg Lys Val Thr Asn Leu Phe Xaa Tyr Glu His Arg Val Asn  
1 5 10 15

Val Cys Glu Leu Xaa Leu Val Asp Asn His Pro Asn Cys Val Val Gln  
           20                          25                          30  
 Ser Tyr Leu Thr Trp Leu Thr Asp Gln Asp Tyr Asp Pro Asn Cys Ser  
           35                          40                          45  
 Leu Cys Lys Thr Thr Leu Xaa Glu Gly Asp Thr Ile Arg Leu Asn Cys  
           50                          55                          60  
 Leu His Leu Leu His Trp Lys Cys Phe Asp Glu Trp Xaa Gly Asn Phe  
           65                          70                          75                          80  
 Pro Asp Thr Thr Ala Pro Xaa Gly Tyr Arg Cys Pro Cys Cys Ser Gln  
                           85                          90                          95  
 Glu Val Phe Pro Pro Asp Gln  
                           100

<210> 50  
 <211> 45  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Cys Asn Ile Pro Leu Ala Ser Arg Glu Thr Thr Arg Leu Val Cys Tyr  
   1                          5                          10                          15  
 Asp Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu Pro  
           20                          25                          30

Arg Asn Thr Ala Pro Ala Gly Tyr Gln Cys Pro Ser Cys  
           35                          40                          45

<210> 51  
 <211> 45  
 <212> PRT  
 <213> C. elegans

<400> 51  
 Cys Ser Ile Cys Leu Glu Asn Lys Asn Pro Ser Ala Leu Phe Cys Gly  
   1                          5                          10                          15  
 His Leu Phe Cys Trp Thr Cys Ile Gln Glu His Ala Val Ala Ala Thr  
           20                          25                          30

Ser Ser Ala Ser Thr Ser Ser Ala Arg Cys Pro Gln Cys  
           35                          40                          45

<210> 52  
 <211> 24  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn

1 5 10 15

Pro Asn Cys Arg Leu Cys Asn Ile  
20

<210> 53

<211> 24

<212> PRT

<213> Saccharomyces pombe

<400> 53

Cys Ala Thr Thr Asn Thr Pro Lys Trp Arg Arg Asp Glu Ser Gly Asn  
1 5 10 15

Pro Ile Cys Asn Ala Cys Gly Leu  
20

<210> 54

<211> 66

<212> PRT

<213> Homo sapiens

<400> 54

Ser Ser Thr Pro Gly Pro Glu Glu Val Asp Ser Ala Ser Ala Ala Pro  
1 5 10 15

Ala Phe Tyr Ser Gln Ala Pro Arg Pro Pro Ala Ser Pro Gly Arg Pro  
20 25 30

Glu Gln His Thr Val Ile His Met Gly Asn Pro Glu Pro Leu Thr His  
35 40 45

Ala Pro Arg Lys Val Tyr Asp Thr Arg Asp Asp Asp Arg Thr Pro Gly  
50 55 60

Leu His  
65

<210> 55

<211> 66

<212> PRT

<213> Saccharomyces pombe

<400> 55

Ala Ser Leu Leu Asn Pro Glu Glu Pro Pro Ser Asn Ser Asp Lys Gln  
1 5 10 15

Pro Ser Met Ser Asn Gly Pro Lys Ser Glu Val Ser Pro Ser Gln Ser  
20 25 30

Gln Gln Ala Pro Leu Ile Gln Ser Ser Thr Ser Pro Val Ser Leu Gln  
35 40 45

Phe Pro Pro Glu Val Gln Gly Ser Asn Val Asp Lys Arg Asn Tyr Ala



50

55

60

Leu Asn

65

&lt;210&gt; 56

&lt;211&gt; 259

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 56

ggcctccctc tgatcgatga ggtggtgagc ccagagcccg agccctcaa cacgtctgac 60  
 ttctctgact ggtctagttt taatgccagc agtaccctg gaccagagga ggtagacagc 120  
 gcctctgctg cccagcctt ctacagccag gccccccggc cccagcttc cccaggccgg 180  
 cccgagcagc acacagtgat ccacatgggc aatcctgagc ccttgactca cgcccctagg 240  
 aaggtgtatg atacgcggg 259

&lt;210&gt; 57

&lt;211&gt; 259

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 57

gggctccctc tgatcgatga ggtgataagc ccagagcccg agccctcaa ttcctcagac 60  
 ttctctgatt ggtccagctt taatgccacc accacctctg tgcaagagga gagagccagc 120  
 actccatctg cacctgcttt ctatagccag gctccccgcc ctctccctc cccaagccgt 180  
 cccgagcagc acacagtcac acacatgggg agtactgaag ccttggcaca cgcccgaagg 240  
 aaagtatatg acacaccgg 259

&lt;210&gt; 58

&lt;211&gt; 55

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 58

gcactgagag agaagctggc cacagtcaac tgggcccggg caggactggg cctcc 55

&lt;210&gt; 59

&lt;211&gt; 55

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

gcactgagag aaaagctagc cacagtcaac ttggccccggg caggactggg ctccc 55

<210> 60  
<211> 44  
<212> DNA  
<213> Homo sapiens

<400> 60  
gccttggtt ggctggcccg gctgctaagg agccgggctg ggtc 44

<210> 61  
<211> 44  
<212> DNA  
<213> Homo sapiens

<400> 61  
gctctgggct ggctggccca gctgctcagg agccgggctg ggtc 44

<210> 62  
<211> 35  
<212> DNA  
<213> Homo sapiens

<400> 62  
ggagactgtg acgatgacaa gtaccgacgt cggcc 35

<210> 63  
<211> 35  
<212> DNA  
<213> Homo sapiens

<400> 63  
ggagactgtg atgatgacaa ataccgccgc cggcc 35

<210> 64  
<211> 32  
<212> DNA  
<213> Homo sapiens

<400> 64  
cgggatgatg accggacacc aggcctccat gg 32

<210> 65  
<211> 32  
<212> DNA  
<213> Homo sapiens

<400> 65

cgggatgatg accggacagc aggcattcat gg

32

<210> 66

<211> 190

<212> DNA

<213> Homo sapiens

<400> 66

cgtctgactt ctctgactgg tctagtttta atgccagcag tacccttgga ccagaggagg 60

tagacagcgc ctctgctgcc ccagccttct acagccaggc cccccggccc ccagcttccc 120

caggccggcc cgagcagcac acagtgatcc acatgggcaa tcctgagccc ttgactcacg 180

cccctaggaa 190

<210> 67

<211> 190

<212> DNA

<213> Homo sapiens

<400> 67

cctcagactt ctctgattgg tccagcttta atgccaccac cacctctgtg caagaggaga 60

gagccagcac tccatctgcg cctgctttct atagccaggc tccccgccct cctccctccc 120

caagccgtcc cgagcagcac acagtcatac acatggggag tactgaagcc ctggcacacg 180

ccccaaggaa 190

<210> 68

<211> 98

<212> DNA

<213> Homo sapiens

<400> 68

gcactgagag agaagctggc cacagtcaac tgggcccggg caggactggg cctccctctg 60

atcgatgagg tggtagagccc agagcccag cccctcaa 98

<210> 69

<211> 98

<212> DNA

<213> Homo sapiens

<400> 69

gcactgagag acaagctagc cacagtcaac tgggcccggg caggactggg cctccctctg 60

atcgatgagg tgataagccc agagcccag cccctcaa 98

<210> 70  
<211> 60  
<212> DNA  
<213> Homo sapiens

<400> 70  
gggatgatga ccggacacca ggctccatg gagactgtga cgatgacaag taccgacgtc 60

<210> 71  
<211> 60  
<212> DNA  
<213> Homo sapiens

<400> 71  
ggattgatga ccggacagca ggcattcatg gagactgtga tgatgacaaa taccgccgcc 60

<210> 72  
<211> 75  
<212> DNA  
<213> Homo sapiens

<400> 72  
taccgccctt cggaaccagt gcagcggccg atcagtaaac acagagactg gggatcgatc 60  
atggggccttt gtaag 75

<210> 73  
<211> 74  
<212> DNA  
<213> Mus musculus

<400> 73  
cttcgcgct ttctattacc gtacgcaccg gtcacgatcg gcatcgcgga ggatcgggtca 60  
tgggactttg caag 74

<210> 74  
<211> 85  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Zinc finger  
consensus.

<220>  
<221> UNSURE  
<222> (2)..(3)  
<223> Xaa at position 2 and 3 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (5)..(8)  
 <223> Xaa at position 5, 6, 7 and 8 can be any amino acid.  
  
 <220>  
 <221> UNSURE  
 <222> (10)..(11)  
 <223> Xaa at position 10 and 11 can be any amino acid.  
  
 <220>  
 <221> UNSURE  
 <222> (13)..(16)  
 <223> Xaa at position 13, 14, 15 and 16 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (18)..(37)  
 <223> Xaa at position 18-37 can be any amino acid.  
  
 <220>  
 <221> UNSURE  
 <222> (39)..(40)  
 <223> Xaa at position 39 and 40 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (42)..(59)  
 <223> Xaa at position 42-59 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (61)..(62)  
 <223> Xaa at position 61 and 62 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (64)..(81)  
 <223> Xaa at position 64-81 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (83)..(84)  
 <223> Xaa at position 83 and 84 can be any amino acid.

<400> 74  
 Cys Xaa Xaa His Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa  
 1 5 10 15  
 His Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30  
 Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 35 40 45  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Cys Xaa  
 50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
65 70 75 80

Xaa Cys Xaa Xaa Cys  
85

<210> 75

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Leucine zipper  
finger consensus.

<220>

<221> UNSURE

<222> (2)..(7)

<223> Xaa at position 2-7 can be any amino acid.

<220>

<221> UNSURE

<222> (9)..(14)

<223> Xaa at position 9-14 can be any amino acid.

<220>

<221> UNSURE

<222> (16)..(21)

<223> Xaa at position 16-21 can be any amino acid.

<220>

<221> UNSURE

<222> (23)..(28)

<223> Xaa at position 23-28 can be any amino acid.

<400> 75

Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Arg Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu  
20 25

<210> 76

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Novel leucine  
zipper finger consensus.

<220>

<221> UNSURE

<222> (2)..(7)

<223> Xaa at position 2-7 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (9)  
 <223> Xaa at position 9 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (11)..(16)  
 <223> Xaa at position 11-16 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (18)  
 <223> Xaa at position 18 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (20)..(25)  
 <223> Xaa at position 20-25 can be any amino acid.

<400> 76  
 Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Leu Xaa Xaa Xaa Xaa Xaa  
     1                    5                    10                    15  
 Leu Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu  
                     20                    25

<210> 77  
 <211> 627  
 <212> PRT  
 <213> C. elegans

<400> 77  
 Met Ser Ser Lys Val Glu Glu Asp Gln His Gln Glu Leu Leu Thr Glu  
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 Asp Gln Leu Val Ala Arg Cys Val Glu Cys Phe Asp Val Asp Glu Glu  
                     20                    25                    30  
 Asp Glu Val Glu Asp Ile Glu Phe Val Asp Ala Leu Phe Leu Ser His  
                     35                    40                    45  
 Gln Trp Leu Ser Asp Ser Leu Ser Leu Ile Thr His Phe Val Asn Phe  
                     50                    55                    60  
 Tyr Gln Glu Thr Arg Asn Val Glu Gln Arg Glu Ala Val Cys Arg Ala  
     65                    70                    75                    80  
 Val Ser Phe Trp Ile Glu Lys Phe Pro Met His Phe Asp Ala Gln Pro  
                     85                    90                    95  
 Gln Val Cys Ala Gln Val Val Arg Leu Lys Thr Ile Ala Glu Asp Ile  
                     100                    105                    110  
 Asn Glu Asn Ile Arg Asn Gly Leu Asp Val Ser Ala Leu Pro Ser Phe  
                     115                    120                    125

Ala Trp Leu Arg Ala Val Ser Val Arg Asn Pro Leu Ala Lys Gln Thr  
 130 135 140  
 Ile Val Arg Val Asp Phe Glu Thr Leu Pro Thr Pro Gly Thr Pro Pro  
 145 150 155 160  
 Pro Phe Pro Ile Ala Ser Lys Lys Phe Ser Leu Thr Ala Phe Ser Leu  
 165 170 175  
 Ser Phe Val Ala Gln Ser Pro Ser Asp Ile Ser Thr Ser Leu Ser His  
 180 185 190  
 Ile Asp Tyr Arg Val Leu Ser Thr Ile Ser Ile Thr Glu Leu Lys Gln  
 195 200 205  
 Tyr Val Lys Asp Gly His Leu Arg Ser Cys Pro Met Leu Glu Arg Ser  
 210 215 220  
 Ile Ser Val Phe Asn Asn Leu Ser Asn Trp Val Gln Cys Leu Ile Leu  
 225 230 235 240  
 Asn Lys Thr Thr Pro Lys Glu Arg Ala Glu Ile Leu Val Lys Phe Val  
 245 250 255  
 His Val Ala Lys His Leu Arg Lys Ile Asn Asn Phe Asn Thr Leu Met  
 260 265 270  
 Ser Val Val Gly Gly Ile Thr His Ser Ser Val Ala Arg Leu Ala Lys  
 275 280 285  
 Thr Tyr Ala Val Leu Ser Asn Asp Ile Lys Lys Glu Leu Thr Gln Leu  
 290 295 300  
 Thr Asn Leu Leu Ser Ala Gln His Asn Phe Cys Glu Tyr Arg Lys Ala  
 305 310 315 320  
 Leu Gly Ala Cys Asn Lys Lys Phe Arg Ile Pro Ile Ile Gly Val His  
 325 330 335  
 Leu Lys Asp Leu Val Ala Ile Asn Cys Ser Gly Ala Asn Phe Glu Lys  
 340 345 350  
 Thr Lys Cys Ile Ser Ser Asp Lys Leu Val Lys Leu Ser Lys Leu Leu  
 355 360 365  
 Ser Asn Phe Leu Val Phe Asn Gln Lys Gly His Asn Leu Pro Glu Met  
 370 375 380  
 Asn Met Asp Leu Ile Asn Thr Leu Lys Val Ser Leu Asp Ile Arg Tyr  
 385 390 395 400  
 Asn Asp Asp Asp Ile Tyr Glu Leu Ser Leu Arg Arg Glu Pro Lys Thr  
 405 410 415  
 Phe Met Asn Phe Glu Pro Ser Arg Gly Leu Val Phe Ala Glu Trp Ala  
 420 425 430  
 Ser Gly Val Thr Val Ala Pro Asp Asn Ala Thr Val Ser Lys His Ile



435					440					445						
Ser	Ala	Met	Val	Asp	Ala	Val	Phe	Lys	His	Tyr	Asp	His	Asp	Arg	Asp	
450					455					460						
Gly	Phe	Ile	Ser	Gln	Glu	Glu	Phe	Gln	Leu	Ile	Ala	Gly	Asn	Phe	Pro	
465					470					475					480	
Phe	Ile	Asp	Ala	Phe	Val	Asn	Ile	Asp	Val	Asp	Met	Asp	Gly	Gln	Ile	
485					490					495						
Ser	Lys	Asp	Glu	Leu	Lys	Thr	Tyr	Phe	Met	Ala	Ala	Asn	Lys	Asn	Thr	
500					505					510						
Lys	Asp	Leu	Arg	Arg	Gly	Phe	Lys	His	Asn	Phe	His	Glu	Thr	Thr	Phe	
515					520					525						
Leu	Thr	Pro	Thr	Thr	Cys	Asn	His	Cys	Asn	Lys	Leu	Leu	Trp	Gly	Ile	
530					535					540						
Leu	Arg	Gln	Gly	Phe	Lys	Cys	Lys	Asp	Cys	Gly	Leu	Ala	Val	His	Ser	
545					550					555					560	
Cys	Cys	Lys	Ser	Asn	Ala	Val	Ala	Glu	Cys	Arg	Arg	Lys	Ser	Ser	Ser	
565					570					575						
Asn	Leu	Thr	Arg	Ala	Ala	Glu	Trp	Phe	Ala	Ser	Pro	Arg	Gly	Ser	Met	
580					585					590						
Arg	Ser	Arg	Ile	Ile	Asn	Thr	Cys	Asn	Asn	Ser	Gly	Ser	Thr	Pro	Asp	
595					600					605						
Glu	Glu	Ile	Gly	Leu	Val	Ser	Leu	Ala	Cys	Glu	Glu	Val	Phe	Glu	Asp	
610					615					620						
Asp Asp Leu																
625																

<210> 78

<211> 530

<212> DNA

<213> Mus musculus

<400> 78

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gagggttaact tgggtcttag cccacctggc accggcagcc atggcgagca ctctggacct 180
ggacaagggg tgcccgtaga ggagctgctc cgtggctgta tcgaagcctt tgatgactct 240
ggaaaggtgc gagatccaca gctagtgcgc atgtttctca tgatgcaccc ctggtacata 300
ccttcctctc agctggcttc gaaactgctc cacttctatc agcaatcccg gaaggacaac 360
tccaattctc tacagatgaa aacgtgtcac ttggtcaggt actggatctc agccttccca 420

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gcagagttcg acttgaaccc agagctggct gaacagatca aggagctgaa ggctctgtta 480  
gaccaagaag ggaaccgcag gcacagcagc ctcatcgaca tcgagagtgt 530

<210> 79  
<211> 720  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (90)..(719)

<400> 79  
cacgcctcgg aagggaggtt tggggtcggt ggtttcacag tgagtgtgtc tgaagccaaa 60

tggtcggaaa ccgttacccg ctctcctag gcc cgg cta gtg ggg acc cca acc 113

Ala Arg Leu Val Gly Thr Pro Thr  
1 5

gcc tgc ggc tgc ccc tcc caa gtt cct ccc tgt tgg cca ggc atc cag 161

Ala Cys Gly Cys Pro Ser Gln Val Pro Pro Cys Trp Pro Gly Ile Gln  
10 15 20

gtc tcc agt ctc cga gct gcg gag aac cca ccg cca cat gcg gct gcc 209

Val Ser Ser Leu Arg Ala Ala Glu Asn Pro Pro Pro His Ala Ala Ala  
25 30 35 40

cct ttc cat tcg acc ctg tgg gga gcc agg ctt ccg ggg ccc cgt tcc 257

Pro Phe His Ser Thr Leu Trp Gly Ala Arg Leu Pro Gly Pro Arg Ser  
45 50 55

tcc tgt gtg aac tgg gcc ccc cgc ccc cat tcc cag aca tca agg ccg 305

Ser Cys Val Asn Trp Ala Pro Arg Pro His Ser Gln Thr Ser Arg Pro  
60 65 70

cgt ctc cag ata gcc acg att tca ttc ctc gct ccc cac agg tcc ctc 353

Arg Leu Gln Ile Ala Thr Ile Ser Phe Leu Ala Pro His Arg Ser Leu  
75 80 85

tcc cca aaa tat tcc cat ctt gtc cta gcc cat ccc cca gac tat ctc 401

Ser Pro Lys Tyr Ser His Leu Val Leu Ala His Pro Pro Asp Tyr Leu  
90 95 100

aag gac cag ctg tcc cca cgc ccc cga cct cca cta ggc ctg tgc cac 449

Lys Asp Gln Leu Ser Pro Arg Pro Arg Pro Pro Leu Gly Leu Cys His  
105 110 115 120

ccg ctg cct gca gga aga cgc ccg gtc ccg ggc cgg gtt agc ccc atg 497  
 Pro Leu Pro Ala Gly Arg Arg Pro Val Pro Gly Arg Val Ser Pro Met  
 125 130 135  
 gga acg cag cgc ctg tgt ggc cgc ggg act caa ggc tgg cct ggc tca 545  
 Gly Thr Gln Arg Leu Cys Gly Arg Gly Thr Gln Gly Trp Pro Gly Ser  
 140 145 150  
 agt gaa cag cac gtc cag gag gcg acc tcg tcc gcg ggt ttg cat tct 593  
 Ser Glu Gln His Val Gln Glu Ala Thr Ser Ser Ala Gly Leu His Ser  
 155 160 165  
 ggg gtg gac gag ctg ggg gtt cgg tcc gag ccc ggt ggg agg ctc ccg 641  
 Gly Val Asp Glu Leu Gly Val Arg Ser Glu Pro Gly Gly Arg Leu Pro  
 170 175 180  
 gag cgc agc ctg ggc cca gcc cac ccc gcg ccg gcg gcc atg gca ggc 689  
 Glu Arg Ser Leu Gly Pro Ala His Pro Ala Pro Ala Ala Met Ala Gly  
 185 190 195 200  
 acc ctg gac ctg gac aag ggc tgc acg gtg g 720  
 Thr Leu Asp Leu Asp Lys Gly Cys Thr Val  
 205 210

<210> 80  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens

<400> 80  
 Ala Arg Leu Val Gly Thr Pro Thr Ala Cys Gly Cys Pro Ser Gln Val  
 1 5 10 15  
 Pro Pro Cys Trp Pro Gly Ile Gln Val Ser Ser Leu Arg Ala Ala Glu  
 20 25 30  
 Asn Pro Pro Pro His Ala Ala Ala Pro Phe His Ser Thr Leu Trp Gly  
 35 40 45  
 Ala Arg Leu Pro Gly Pro Arg Ser Ser Cys Val Asn Trp Ala Pro Arg  
 50 55 60  
 Pro His Ser Gln Thr Ser Arg Pro Arg Leu Gln Ile Ala Thr Ile Ser  
 65 70 75 80  
 Phe Leu Ala Pro His Arg Ser Leu Ser Pro Lys Tyr Ser His Leu Val  
 85 90 95  
 Leu Ala His Pro Pro Asp Tyr Leu Lys Asp Gln Leu Ser Pro Arg Pro  
 100 105 110

Arg Pro Pro Leu Gly Leu Cys His Pro Leu Pro Ala Gly Arg Arg Pro  
           115                          120                          125  
 Val Pro Gly Arg Val Ser Pro Met Gly Thr Gln Arg Leu Cys Gly Arg  
           130                          135                          140  
 Gly Thr Gln Gly Trp Pro Gly Ser Ser Glu Gln His Val Gln Glu Ala  
   145                          150                          155                          160  
 Thr Ser Ser Ala Gly Leu His Ser Gly Val Asp Glu Leu Gly Val Arg  
                           165                          170                          175  
 Ser Glu Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly Pro Ala His  
                           180                          185                          190  
 Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp Lys Gly Cys  
           195                          200                          205  
 Thr Val  
       210

<210> 81  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 81  
 Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu Glu Val  
   1                          5                          10                          15  
 Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp Arg Asp  
                           20                          25                          30  
 Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val Glu Leu Ser Glu Ala  
           35                          40                          45  
 Tyr Arg Val Leu Ser Arg Glu Ser Arg Arg Ser Tyr Asp  
       50                          55                          60

<210> 82  
 <211> 62  
 <212> PRT  
 <213> C. elegans

<400> 82  
 Tyr Tyr Glu Ile Leu Gly Val Ser Lys Thr Ala Glu Glu Arg Glu Ile  
   1                          5                          10                          15  
 Arg Lys Ala Tyr Lys Arg Leu Ala Met Lys Tyr His Pro Asp Arg Asn  
           20                          25                          30  
 Gln Gly Asp Lys Glu Ala Glu Ala Lys Phe Lys Glu Ile Lys Glu Ala  
       35                          40                          45

Tyr Glu Val Leu Thr Asp Ser Gln Lys Arg Ala Ala Tyr Asp  
50 55 60

<210> 83  
<211> 37  
<212> PRT  
<213> Homo sapiens

<400> 83  
Gln Arg Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro  
1 5 10 15

Gly Ala Ser Thr Glu Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys  
20 25 30

Glu Leu His Pro Asp  
35

<210> 84  
<211> 37  
<212> PRT  
<213> C. elegans

<400> 84  
Lys Lys Ile Arg Gln Arg Thr His Tyr Glu Val Leu Gly Val Glu Ser  
1 5 10 15

Thr Ala Thr Leu Ser Glu Ile Lys Ser Ala Phe Tyr Ala Gln Ser Lys  
20 25 30

Lys Val His Pro Asp  
35

<210> 85  
<211> 32  
<212> PRT  
<213> Homo sapiens

<400> 85  
Ser Leu His Ser Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu  
1 5 10 15

Ser Arg Glu Gln Ser Arg Arg Ser Tyr Asp Asp Gln Leu Arg Ser Gly  
20 25 30

<210> 86  
<211> 32  
<212> PRT  
<213> C. elegans

<400> 86  
Ser Ala Thr Ala Ser Phe Leu Glu Leu Lys Asn Ala Tyr Asp Val Leu  
1 5 10 15

Arg Arg Pro Ala Asp Arg Arg Leu Tyr Asp Tyr Gln Leu Arg Gly Gly  
                   20                                  25                                  30

<210> 87  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 87  
 Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile Ala Phe Arg Lys  
   1                                  5                                  10                                  15  
 Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys Asp Arg Ile Ile  
                   20                                  25                                  30  
 Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg  
                   35                                  40

<210> 88  
 <211> 42  
 <212> PRT  
 <213> C. elegans

<400> 88  
 Leu Val Leu Val Ala Gly Tyr Asn Gly Gly Tyr Leu Tyr Leu Leu Ala  
   1                                  5                                  10                                  15  
 Tyr Asn Gln Lys Gln Leu Asp Lys Leu Ile Asp Glu Asp Glu Ile Ala  
                   20                                  25                                  30  
 Lys Cys Phe Leu Arg Gln Lys Glu Phe Arg  
                   35                                  40

<210> 89  
 <211> 41  
 <212> PRT  
 <213> Homo sapiens

<400> 89  
 Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu Glu Val  
   1                                  5                                  10                                  15  
 Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp Arg Asp  
                   20                                  25                                  30  
 Pro Gly Asn Pro Ser Leu His Ser Arg  
                   35                                  40

<210> 90  
 <211> 41  
 <212> PRT

<213> C. elegans

<400> 90

Tyr Tyr Glu Ile Ile Gly Val Ser Ala Ser Ala Thr Arg Gln Glu Ile  
1 5 10 15

Arg Asp Ala Phe Leu Lys Lys Thr Lys Gln Leu His Pro Asp Gln Ser  
20 25 30

Arg Lys Ser Ser Lys Ser Asp Ser Arg  
35 40

<210> 91

<211> 22

<212> PRT

<213> Homo sapiens

<400> 91

Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln  
1 5 10 15

Ser Arg Arg Ser Tyr Asp  
20

Bb <210> 92

<211> 22

<212> PRT

<213> C. elegans

<400> 92

Gln Phe Met Leu Val Lys Glu Ala Tyr Asp Val Leu Arg Asn Glu Glu  
1 5 10 15

Lys Arg Lys Glu Tyr Asp  
20

<210> 93

<211> 44

<212> PRT

<213> Homo sapiens

<400> 93

Gln Gly Pro Gln Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln Val  
1 5 10 15

Leu Gly Tyr Cys Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr  
20 25 30

Ile Ala Phe Arg Lys Val Lys Gln Met His Leu Asn  
35 40

<210> 94

<211> 44

<212> PRT

<213> C. elegans

<400> 94

Arg	Asn	Pro	Glu	Asp	Glu	Tyr	Leu	Arg	Glu	Lys	Trp	Lys	Asn	Arg	Met
1				5					10					15	
Leu	Val	Val	Leu	Ala	Ala	Thr	Val	Met	Ala	Leu	Ile	Gly	Ala	Asn	Ile
			20					25					30		
Val	Tyr	Ile	Arg	Lys	Leu	Gln	Ala	Asp	Arg	Leu	Ser				
		35					40								

<210> 95

<211> 36

<212> PRT

<213> Homo sapiens

<400> 95

Tyr	Tyr	Glu	Leu	Leu	Gly	Val	His	Pro	Gly	Ala	Ser	Thr	Glu	Glu	Val
1				5					10					15	
Lys	Arg	Ala	Phe	Phe	Ser	Lys	Ser	Lys	Glu	Leu	His	Pro	Asp	Arg	Asp
			20					25					30		
Pro	Gly	Asn	Pro												
		35													

<210> 96

<211> 36

<212> PRT

<213> S. pombe

<400> 96

Tyr	Tyr	Asp	Leu	Leu	Gly	Ile	Ser	Thr	Asp	Ala	Thr	Ala	Val	Asp	Ile
1				5					10					15	
Lys	Lys	Ala	Tyr	Arg	Lys	Leu	Ala	Val	Lys	Tyr	His	Pro	Asp	Lys	Asn
			20					25					30		
Pro	Asp	Asp	Pro												
		35													

<210> 97

<211> 40

<212> PRT

<213> Homo sapiens

<400> 97

Arg	Phe	Val	Glu	Leu	Ser	Glu	Ala	Tyr	Arg	Val	Leu	Ser	Arg	Glu	Gln
1				5					10					15	
Ser	Arg	Arg	Ser	Tyr	Asp	Asp	Gln	Leu	Arg	Ser	Gly	Ser	Pro	Pro	Lys
			20					25					30		



Ser Pro Arg Thr Thr Val His Asp  
35 40

<210> 98  
<211> 40  
<212> PRT  
<213> S. pombe

<400> 98  
Lys Phe Gln Lys Ile Ser Glu Ala Tyr Gln Val Leu Gly Asp Glu Lys  
1 5 10 15

Bb Leu Arg Ser Gln Tyr Asp Gln Phe Gly Lys Glu Lys Ala Val Pro Glu  
20 25 30

Gln Gly Phe Thr Asp Ala Tyr Asp  
35 40

<210> 99  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 99  
Asp Arg Ile Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg  
1 5 10 15

Ala Asn Arg Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu  
20 25

<210> 100  
<211> 29  
<212> PRT  
<213> S. pombe

<400> 100

Asp Arg Lys Lys Asn Ala Gln Ile Arg Glu Arg Glu Ala Leu Ala Lys  
1 5 10 15

Arg Glu Gln Glu Met Ile Glu Asp Arg Arg Gln Arg Ile  
20 25

<210> 101  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 101  
Pro Gln Gly Pro Gln Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln  
1 5 10 15

Val Leu Gly

<210> 102  
 <211> 19  
 <212> PRT  
 <213> *S. pombe*

<400> 102  
 Pro Gln Gly Ala Ser Glu Lys Phe Gln Lys Ile Ser Glu Ala Tyr Gln  
           1                  5                  10                  15

Val Leu Gly

<210> 103  
 <211> 71  
 <212> PRT  
 <213> *Homo sapiens*

<400> 103  
 Ala Gly Gln Arg Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu Gly Val  
           1                  5                  10                  15

His Pro Gly Ala Ser Thr Glu Glu Val Lys Arg Ala Phe Phe Ser Lys  
                   20                  25                  30

Ser Lys Glu Leu His Pro Asp Arg Asp Pro Gly Asn Pro Ser Leu His  
           35                  40                  45

Ser Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu  
           50                  55                  60

Gln Ser Arg Arg Ser Tyr Asp  
           65                  70

<210> 104  
 <211> 71  
 <212> PRT  
 <213> *Drosophila virilis*

<400> 104  
 Ser Ser Ser Arg Met Gln Ala Lys Asp Tyr Tyr Ala Thr Leu Gly Val  
           1                  5                  10                  15

Ala Lys Asn Ala Asn Ala Lys Asp Ile Lys Lys Ala Tyr Tyr Glu Leu  
                   20                  25                  30

Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp Pro Asp Ala Ser  
           35                  40                  45

Lys Lys Phe Gln Asp Val Ser Glu Ala Tyr Glu Val Leu Ser Asp Asp  
           50                  55                  60

Gln Lys Arg Arg Glu Tyr Asp  
           65                  70

<210> 105  
 <211> 397  
 <212> PRT  
 <213> Homo sapiens

<400> 105

Met	Val	Lys	Glu	Thr	Thr	Tyr	Tyr	Asp	Val	Leu	Gly	Val	Lys	Pro	Asn
1				5					10					15	
Ala	Thr	Gln	Glu	Glu	Leu	Lys	Lys	Ala	Tyr	Arg	Lys	Leu	Ala	Leu	Lys
		20						25					30		
Tyr	His	Pro	Asp	Lys	Asn	Pro	Asn	Glu	Gly	Glu	Lys	Phe	Lys	Gln	Ile
		35					40					45			
Ser	Gln	Ala	Tyr	Glu	Val	Leu	Ser	Asp	Ala	Lys	Lys	Arg	Glu	Leu	Tyr
	50					55					60				
Asp	Lys	Gly	Gly	Glu	Gln	Ala	Ile	Lys	Glu	Gly	Gly	Ala	Gly	Gly	Gly
65					70					75					80
Phe	Gly	Ser	Pro	Met	Asp	Ile	Phe	Asp	Met	Phe	Phe	Gly	Gly	Gly	Gly
				85					90					95	
Arg	Met	Gln	Arg	Glu	Arg	Arg	Gly	Lys	Asn	Val	Val	His	Gln	Leu	Ser
		100						105					110		
Val	Thr	Leu	Glu	Asp	Leu	Tyr	Asn	Gly	Ala	Thr	Arg	Lys	Leu	Ala	Leu
		115					120					125			
Gln	Lys	Asn	Val	Ile	Cys	Asp	Lys	Cys	Glu	Gly	Arg	Gly	Gly	Lys	Lys
	130					135					140				
Gly	Ala	Val	Glu	Cys	Cys	Pro	Asn	Cys	Arg	Gly	Thr	Gly	Met	Gln	Ile
145					150					155					160
Arg	Ile	His	Gln	Ile	Gly	Pro	Gly	Met	Val	Gln	Gln	Ile	Gln	Ser	Val
			165					170						175	
Cys	Met	Glu	Cys	Gln	Gly	His	Gly	Glu	Arg	Ile	Ser	Pro	Lys	Asp	Arg
		180						185					190		
Cys	Lys	Ser	Cys	Asn	Gly	Arg	Lys	Ile	Val	Arg	Glu	Lys	Lys	Ile	Leu
		195					200					205			
Glu	Val	His	Ile	Asp	Lys	Gly	Met	Lys	Asp	Gly	Gln	Lys	Ile	Thr	Phe
	210					215					220				
His	Gly	Glu	Gly	Asp	Gln	Glu	Pro	Gly	Leu	Glu	Pro	Gly	Asp	Ile	Ile
225					230					235					240
Ile	Val	Leu	Asp	Gln	Lys	Asp	His	Ala	Val	Phe	Thr	Arg	Arg	Gly	Glu
			245						250					255	
Asp	Leu	Phe	Met	Cys	Met	Asp	Ile	Gln	Leu	Val	Glu	Ala	Leu	Cys	Gly
		260						265					270		
Phe	Gln	Lys	Pro	Ile	Ser	Thr	Leu	Asp	Asn	Arg	Thr	Ile	Val	Ile	Thr

275	280	285
Ser His Pro Gly Gln Ile Val Lys His Gly Asp Ile Lys Cys Val Leu		
290	295	300
Asn Glu Gly Met Pro Ile Tyr Arg Arg Pro Tyr Glu Lys Gly Arg Leu		
305	310	315
Ile Ile Glu Phe Lys Val Asn Phe Pro Glu Asn Gly Phe Leu Ser Pro		
	325	330
Asp Lys Leu Ser Leu Leu Glu Lys Leu Leu Pro Glu Arg Lys Glu Val		
	340	345
Glu Glu Thr Asp Glu Met Asp Gln Val Glu Leu Val Asp Phe Asp Pro		
	355	360
Asn Gln Glu Arg Arg Arg His Tyr Asn Gly Glu Ala Tyr Glu Asp Asp		
	370	375
		380
Glu His His Pro Arg Gly Gly Val Gln Cys Gln Thr Ser		
385	390	395
<210> 106		
<211> 340		
<212> PRT		
<213> Homo sapiens		
<400> 106		
Met Gly Lys Asp Tyr Tyr Gln Thr Leu Gly Leu Ala Arg Gly Ala Ser		
1	5	10
		15
Asp Glu Glu Ile Lys Arg Ala Tyr Arg Arg Gln Ala Leu Arg Tyr His		
	20	25
		30
Pro Asp Lys Asn Lys Glu Pro Gly Ala Glu Glu Lys Phe Lys Glu Ile		
	35	40
		45
Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Arg Lys Arg Glu Ile Phe		
	50	55
		60
Asp Arg Tyr Gly Glu Glu Gly Leu Lys Gly Ser Gly Pro Ser Gly Gly		
	65	70
		75
Ser Gly Gly Gly Ala Asn Gly Thr Ser Phe Ser Tyr Thr Phe His Gly		
	85	90
		95
Asp Pro His Ala Met Phe Ala Glu Phe Phe Gly Gly Arg Asn Pro Phe		
	100	105
		110
Asp Thr Phe Phe Gly Gln Arg Asn Gly Glu Glu Gly Met Asp Ile Asp		
	115	120
		125
Asp Pro Phe Ser Gly Phe Pro Met Gly Met Gly Gly Phe Thr Asn Val		
	130	135
		140

Asn Phe Gly Arg Ser Arg Ser Ala Gln Glu Pro Ala Arg Lys Lys Gln  
 145 150 155 160  
 Asp Pro Pro Val Thr His Asp Leu Arg Val Ser Leu Glu Glu Ile Tyr  
 165 170 175  
 Ser Gly Cys Thr Lys Lys Met Lys Ile Ser His Lys Arg Leu Asn Pro  
 180 185 190  
 Asp Gly Lys Ser Ile Arg Asn Glu Asp Lys Ile Leu Thr Ile Glu Val  
 195 200 205  
 Lys Lys Gly Trp Lys Glu Gly Thr Lys Ile Thr Phe Pro Lys Glu Gly  
 210 215 220  
 Asp Gln Thr Ser Asn Asn Ile Pro Ala Asp Ile Val Phe Val Leu Lys  
 225 230 235 240  
 Asp Lys Pro His Asn Ile Phe Lys Arg Asp Gly Ser Asp Val Ile Tyr  
 245 250 255  
 Pro Ala Arg Ile Ser Leu Arg Glu Ala Leu Cys Gly Cys Thr Val Asn  
 260 265 270  
 Val Pro Thr Leu Asp Gly Arg Thr Ile Pro Val Val Phe Lys Asp Val  
 275 280 285  
 Ile Arg Pro Gly Met Arg Arg Lys Val Pro Gly Glu Gly Leu Pro Leu  
 290 295 300  
 Pro Lys Thr Pro Glu Lys Arg Gly Asp Leu Ile Ile Glu Phe Glu Val  
 305 310 315 320  
 Ile Phe Pro Glu Arg Ile Pro Gln Thr Ser Arg Thr Val Leu Glu Gln  
 325 330 335  
 Val Leu Pro Ile  
 340

<210> 107

<211> 351

<212> PRT

<213> Homo sapiens

<400> 107

Met Ala Ser Tyr Tyr Glu Ile Leu Asp Val Pro Arg Ser Ala Ser Ala  
 1 5 10 15  
 Asp Asp Ile Lys Lys Ala Tyr Arg Arg Lys Ala Leu Gln Trp His Pro  
 20 25 30  
 Asp Lys Asn Pro Asp Asn Lys Glu Phe Ala Glu Lys Lys Phe Lys Glu  
 35 40 45



<210> 108  
 <211> 848  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (30)..(764)

<400> 108  
 caaggagcct ctgcctgccc gtcgtcgtc atg ccg tcc ctg ttg ctc cag ctg 53  
 Met Pro Ser Leu Leu Leu Gln Leu  
 1 5  
 ccc ctg cgc cta tgc cgg ctg tgg ccg cat agc ctt tcc atc cga ctt 101  
 Pro Leu Arg Leu Cys Arg Leu Trp Pro His Ser Leu Ser Ile Arg Leu  
 10 15 20  
 ctc aca gcc gcc aca ggg cag cgg tct gtc cct act aat tac tat gaa 149  
 Leu Thr Ala Ala Thr Gly Gln Arg Ser Val Pro Thr Asn Tyr Tyr Glu  
 25 30 35 40  
 ttg ttg ggc gtg cat ccg ggt gcc agc gct gaa gag att aaa cgt gct 197  
 Leu Leu Gly Val His Pro Gly Ala Ser Ala Glu Glu Ile Lys Arg Ala  
 45 50 55  
 ttt ttc acc aag tca aaa gag cta cac cct gat cga gac cct ggg aac 245  
 Phe Phe Thr Lys Ser Lys Glu Leu His Pro Asp Arg Asp Pro Gly Asn  
 60 65 70  
 cca gcc ctg cat agc cgc ttt gtg gag ctg aat gag gca tat cga gtg 293  
 Pro Ala Leu His Ser Arg Phe Val Glu Leu Asn Glu Ala Tyr Arg Val  
 75 80 85  
 ctc agt cgt gag gaa agt cgt cgt aac tat gac cac cag ctg cat tca 341  
 Leu Ser Arg Glu Glu Ser Arg Arg Asn Tyr Asp His Gln Leu His Ser  
 90 95 100  
 gcc agt cct cca aag tct tca ggg agc aca gcc gag cct aag tat acg 389  
 Ala Ser Pro Pro Lys Ser Ser Gly Ser Thr Ala Glu Pro Lys Tyr Thr  
 105 110 115 120  
 caa cag aca cac agc agc tcc tgg gaa ccc ccc aac gct caa tac tgg 437  
 Gln Gln Thr His Ser Ser Ser Trp Glu Pro Pro Asn Ala Gln Tyr Trp  
 125 130 135  
 gcc cag ttc cac agt gtg agg ccg cag ggg ccg gag tca agg aag cag 485  
 Ala Gln Phe His Ser Val Arg Pro Gln Gly Pro Glu Ser Arg Lys Gln

140	145	150	
cag cgt aaa cac aac cag cgg gtc ctg ggg tac tgc ctc ctg ctc atg			533
Gln Arg Lys His Asn Gln Arg Val Leu Gly Tyr Cys Leu Leu Leu Met			
155	160	165	
gtg gca ggc atg ggc ctg cac tat gtt gcc ttc agg aag ctg gag cag			581
Val Ala Gly Met Gly Leu His Tyr Val Ala Phe Arg Lys Leu Glu Gln			
170	175	180	
gtg cat cgc agc ttc atg gat gaa aag gac cgg atc att aca gcc atc			629
Val His Arg Ser Phe Met Asp Glu Lys Asp Arg Ile Ile Thr Ala Ile			
185	190	195	200
tac aat gac act cgg gcc agg gcc agg gcc aac aga gcc agg att cag			677
Tyr Asn Asp Thr Arg Ala Arg Ala Arg Ala Asn Arg Ala Arg Ile Gln			
205	210	215	
cag gag cgc cac gag agg cag cag cct cgg gca gaa ccc tcc ctg cct			725
Gln Glu Arg His Glu Arg Gln Gln Pro Arg Ala Glu Pro Ser Leu Pro			
220	225	230	
cca gaa agc tcc agg atc atg ccc cag gac aca agc ccc tgagaggctt			774
Pro Glu Ser Ser Arg Ile Met Pro Gln Asp Thr Ser Pro			
235	240	245	
aactaaatgg gaccttcatt ggtcctctcc ctgctgctg tccagaacta cacgtgcaat			834
aaactcattt tcag			848

<210> 109

<211> 245

<212> PRT

<213> Mus musculus

<400> 109

Met Pro Ser Leu Leu Leu Gln Leu Pro Leu Arg Leu Cys Arg Leu Trp			
1	5	10	15
Pro His Ser Leu Ser Ile Arg Leu Leu Thr Ala Ala Thr Gly Gln Arg			
20	25	30	
Ser Val Pro Thr Asn Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala			
35	40	45	
Ser Ala Glu Glu Ile Lys Arg Ala Phe Phe Thr Lys Ser Lys Glu Leu			
50	55	60	
His Pro Asp Arg Asp Pro Gly Asn Pro Ala Leu His Ser Arg Phe Val			



65	70	75	80
Glu Leu Asn Glu Ala Tyr Arg Val Leu Ser Arg Glu Glu Ser Arg Arg	85	90	95
Asn Tyr Asp His Gln Leu His Ser Ala Ser Pro Pro Lys Ser Ser Gly	100	105	110
Ser Thr Ala Glu Pro Lys Tyr Thr Gln Gln Thr His Ser Ser Ser Trp	115	120	125
Glu Pro Pro Asn Ala Gln Tyr Trp Ala Gln Phe His Ser Val Arg Pro	130	135	140
Gln Gly Pro Glu Ser Arg Lys Gln Gln Arg Lys His Asn Gln Arg Val	145	150	155
Leu Gly Tyr Cys Leu Leu Leu Met Val Ala Gly Met Gly Leu His Tyr	165	170	175
Val Ala Phe Arg Lys Leu Glu Gln Val His Arg Ser Phe Met Asp Glu	180	185	190
Lys Asp Arg Ile Ile Thr Ala Ile Tyr Asn Asp Thr Arg Ala Arg Ala	195	200	205
Arg Ala Asn Arg Ala Arg Ile Gln Gln Glu Arg His Glu Arg Gln Gln	210	215	220
Pro Arg Ala Glu Pro Ser Leu Pro Pro Glu Ser Ser Arg Ile Met Pro	225	230	235
Gln Asp Thr Ser Pro	245		

<210> 110

<211> 120

<212> DNA

<213> Homo sapiens

<400> 110

ttgaagtcta gccccatcct ggtccaatgc gctcttggtta gcctcctttc ccagctgccc 60

gcccgcgcgc atgccgcct tactgccct gcgcctgtg ccggctgtgg ccccgaaccc 120

<210> 111

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: The amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:20.

<400> 111  
Glu Phe Gly Thr Ser  
1 5

<210> 112  
<211> 12  
<212> PRT  
<213> Homo sapiens

<400> 112  
His Thr Pro Gln Gly Lys Val Tyr Asp Thr Arg Asp  
1 5 10

<210> 113  
<211> 38  
<212> PRT  
<213> Homo sapiens

<220>  
<221> UNSURE  
<222> (4)  
<223> Xaa at position 4 can be any amino acid

<220>  
<221> UNSURE  
<222> (35)  
<223> Xaa at position 35 can be any amino acid

<400> 113  
Ala Leu Arg Xaa Lys Leu Ala Thr Val Asn Trp Ala Arg Ala Gly Leu  
1 5 10 15

Gly Leu Pro Leu Ile Asp Glu Val Ile Ser Pro Glu Pro Glu Pro Leu  
20 25 30

Asn Ser Xaa Arg Leu Leu  
35

<210> 114  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 114  
Leu Val Gln Leu  
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<210> 115  
<211> 20  
<212> PRT  
<213> Homo sapiens

<400> 115  
Cys His His His Leu Cys Ala Arg Gly Glu Ser Gln His Ser Ile Cys

1                      5                      10                      15

Ala Cys Phe Leu  
20

<210> 116  
<211> 23  
<212> PRT  
<213> Homo sapiens

<400> 116  
Pro Gly Ser Pro Pro Ser Ser Leu Pro Lys Pro Ser Arg Ala Ala His  
1                      5                      10                      15

Ser His Thr His Gly Glu Tyr  
20

<210> 117  
<211> 33  
<212> PRT  
<213> Homo sapiens

<400> 117  
Ser Pro Gly Thr Arg Pro Lys Glu Lys Tyr Met Thr His Gly Ile Asp  
1                      5                      10                      15

Asp Arg Thr Ala Gly Ile His Gly Asp Cys Asp Asp Asp Lys Tyr Arg  
20                      25                      30

Arg

<210> 118  
<211> 72  
<212> PRT  
<213> Homo sapiens

<400> 118  
Ala Gln Ser Pro Ser Pro Ser Ile Pro Ser Asp Phe Ser Asp Trp Ser  
1                      5                      10                      15

Ser Phe Asn Ala Thr Thr Thr Ser Val Gln Glu Glu Arg Ala Ser Thr  
20                      25                      30

Pro Ser Ala Pro Ala Phe Tyr Ser Gln Ala Pro Arg Pro Pro Pro Ser  
35                      40                      45

Pro Ser Arg Pro Glu Gln His Thr Val Ile His Met Gly Ser Thr Glu  
50                      55                      60

Ala Leu Ala His Ala Pro Arg Lys  
65                      70

<210> 119  
<211> 87

<212> PRT  
<213> Homo sapiens

<400> 119

Gly Leu Pro Leu Ile Asp Glu Val Ile Ser Pro Glu Pro Glu Pro Leu  
1 5 10 15

Asn Ser Ser Asp Phe Ser Asp Trp Ser Ser Phe Asn Ala Thr Thr Thr  
20 25 30

Ser Val Gln Glu Glu Arg Ala Ser Thr Pro Ser Ala Pro Ala Phe Tyr  
35 40 45

Ser Gln Ala Pro Arg Pro Pro Pro Ser Pro Ser Arg Pro Glu Gln His  
50 55 60

Thr Val Ile His Met Gly Ser Thr Glu Ala Leu Ala His Ala Pro Arg  
65 70 75 80

Lys Val Tyr Asp Thr Pro Gly  
85

<210> 120

<211> 34

<212> PRT

<213> Homo sapiens

<400> 120

Pro Asp Ser Arg His Ser Trp Glu Thr Val Met Met Thr Asn Thr Ala  
1 5 10 15

Ala Gly Leu Ala Leu Gly Trp Leu Ala Gln Leu Leu Arg Ser Arg Ala  
20 25 30

Gly Ser

<210> 121

<211> 19

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (11)

<223> Xaa at position 11 can be any amino acid

<400> 121

Ala Leu Arg Glu Lys Leu Ala Thr Val Asn Xaa Ala Arg Ala Gly Leu  
1 5 10 15

Gly Ser Leu

<210> 122

<211> 87  
<212> PRT  
<213> Homo sapiens

<220>  
<221> UNSURE  
<222> (35)  
<223> Xaa at position 35 can be any amino acid

<400> 122  
Ala Gln Ser Pro Ser Pro Ser Ile Pro Gln Thr Ser Leu Ile Gly Pro  
1 5 10 15  
Ala Leu Met Pro Pro Pro Pro Leu Cys Lys Arg Arg Glu Pro Ala Leu  
20 25 30  
His Leu Xaa Leu Leu Ser Ile Ala Arg Leu Pro Ala Leu Leu Pro Pro  
35 40 45  
Gln Ala Val Pro Ser Ser Thr Gln Ser Tyr Thr Trp Gly Val Leu Lys  
50 55 60  
Pro Trp His Thr Pro Gln Gly Lys Tyr Met Thr His Arg Asp Asp Asp  
65 70 75 80  
Arg Thr Ala Gly Ile His Gly  
85

<210> 123  
<211> 20  
<212> PRT  
<213> Homo sapiens

<400> 123  
Pro Pro Ser Ser Leu Pro Lys Pro Ser Arg Ala Ala His Ser His Thr  
1 5 10 15  
His Gly Glu Tyr  
20

<210> 124  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 124  
Ser Pro Gly Thr Arg Pro Lys Glu Ser Ile  
1 5 10

<210> 125  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 125  
His Thr Gly Met Met Thr Gly Gln Gln Ala Phe Met Gly Asp Cys Asp

1

5

10

15

Asp Asp Lys Tyr Arg Arg Arg Pro Cys Ser Gly Leu Ala  
20 25

B6  
concur